

Introduction to High Performance Computing

GSND 5345Q, FDS

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Section 1

Introduction to High Performance Computing

Acknowledgments

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In addition, some information was obtained from the following online slides ([click here](#)).

What is High Performance Computing?

High Performance Computing (HPC) is the use of parallel processing for running advanced application programs efficiently, reliably, and quickly. It involves aggregating computing power in a way that delivers much higher performance than a typical desktop or workstation.

Why High Performance Computing?

- HPC allows users to tackle complex problems that require substantial computational resources.
- It enables simulations, data analysis, and modeling that would be infeasible on standard computers.
- Applications include weather forecasting, molecular modeling, financial modeling, and more.

HPC at Rutgers University

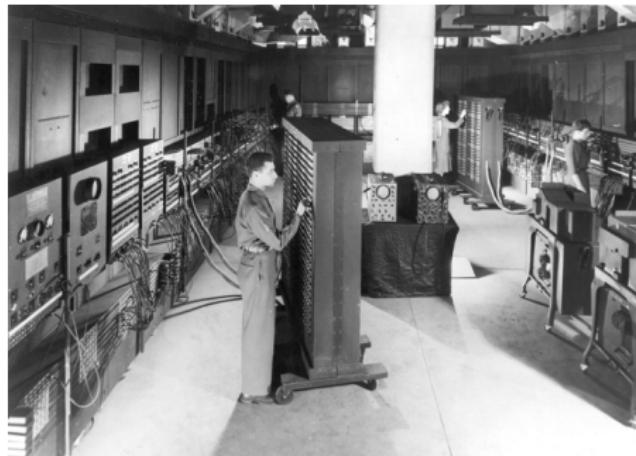
At Rutgers, the primary HPC resources are governed by the Rutgers Office of Advanced Research and Computing (OARC). They provide significant online and synchronous (in person) resources for HPC, along with training in batch submission, programming languages, parallel programming, distributed systems, and HPC architectures.

Section 2

History of High-Performance Computing

Early Beginnings

1940s-1950s: The origins of HPC can be traced back to the development of early computers, such as the ENIAC (Electronic Numerical Integrator and Computer) and UNIVAC (Universal Automatic Computer).



Used for military (cracking Nazi codes) and scientific purposes, including calculations for atomic bomb development and weather forecasting.

Emergence of Supercomputers

1960s-1970s: The concept of supercomputers emerged with machines like the CDC 6600 and Cray-1.



These systems introduced vector processing and specialized architectures optimized for scientific and engineering applications.

Parallel Processing and Clusters

Seymore Cray was an American electrical engineer and supercomputer architect who designed a series of computers that were the fastest in the world for decades, and founded **Cray Research** which built many of these machines. He is often called “the father of supercomputing,” and has been credited with creating the supercomputer industry.

However, Cray resisted the massively parallel solution to high-speed computing, offering a variety of reasons that it would never work as well as one very fast processor. He famously quipped “If you were plowing a field, which would you rather use: two strong oxen or 1024 chickens?”

AI in Medicine at Rutgers



Parallel Processing and Clusters

1980s-1990s: During the speed in supercomputers was primarily achieved through two mechanisms:

- **Vector processors:** these were designed using a pipeline architecture to rapidly perform a single floating point operation on a large amount of data. Achieving high performance depended on data arriving in the processing unit in an uninterrupted stream.
- **Shared memory multiprocessing:** a small number (up to 8) processors with access to the same memory space. Interprocess communication took place via the shared memory.

Parallel Processing and Clusters

1980s-1990s: Parallel processing became a key focus in HPC, leading to the development of massively parallel supercomputers like the Connection Machine and Thinking Machines CM-5.

- Clusters of commodity hardware also gained popularity due to their cost-effectiveness and scalability.
- Memory contention was a major impediment to increasing speed; the vector processors required high-speed access to memory but multiple processors working simultaneously created contention for memory that reduced access speed.
- Vector processing worked well with 4 or 8 processors, but memory contention would prevent a 64 or 128 processor machine from working efficiently.

Evolution of HPC Architectures

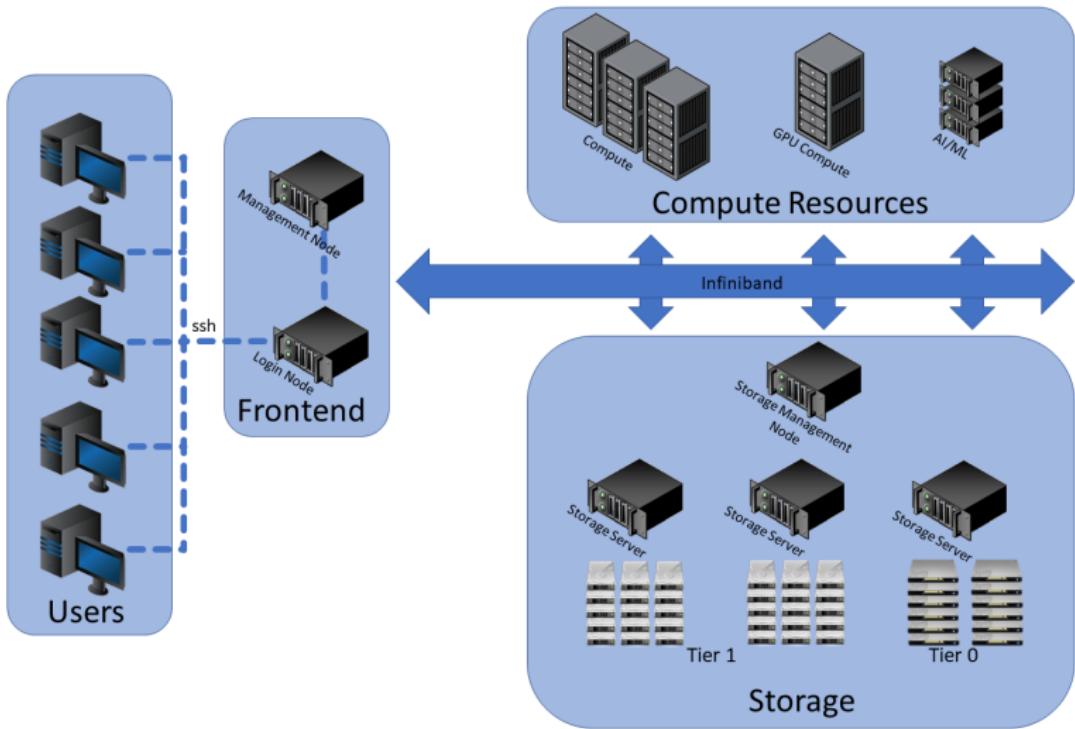
- **2000s-Present:** HPC architectures continue to evolve with the rise of multi-core processors, accelerators (e.g., GPUs), and specialized interconnects. Most universities develop their own HPC resources.



Key Components of High Performance Computing

- ① **Hardware:** Specialized computing infrastructure, including clusters, supercomputers, and accelerators like GPUs.
- ② **Software:** Tools and libraries for parallel programming, job scheduling, and performance optimization.
- ③ **Networking:** High-speed interconnections for data exchange between computing nodes.
- ④ **Parallel Programming Models:** Frameworks and languages for writing parallel applications, such as MPI, OpenMP, and CUDA.

Typical HPC Architecture



Getting Started with High Performance Computing

- ① **Learn Parallel Programming:** Understand parallel programming models and techniques.
- ② **Access to HPC Resources:** Utilize computing clusters or cloud-based HPC services.
- ③ **Optimize Code:** Write efficient code and utilize performance profiling tools.
- ④ **Collaborate and Learn:** Engage with HPC communities, attend workshops, and collaborate with experienced users.

Future Trends

- **Usability and Access:** Interactive and online resources such as OnDemand have made HPC more accessible. Also, cloud computing such as the Google and Amazon Clouds have made HPC accessible to groups and companies (large and small).
- **Exascale Computing:** Efforts are underway to achieve exascale computing, capable of performing 10^{18} floating point operations per second (FLOPS), with projects like the US Department of Energy's Exascale Computing Project.
- **Heterogeneous Architectures:** Continued focus on heterogeneous architectures combining CPUs, GPUs, and accelerators to optimize performance for specific workloads.
- **AI and Machine Learning:** Integration of artificial intelligence (AI) and machine learning techniques into HPC workflows for data analysis, optimization, and predictive modeling.

Section 3

Introduction to the Amarel HPC Cluster

HPC at Rutgers

About Amarel

In July 2017, the [Office of Advanced Research Computing](#) (OARC) unveiled Amarel, a "condominium" style computing environment developed to serve the university's wide-ranging research needs. The Amarel cluster provides a shared platform that optimizes resources for the benefit of all users. Named in honor of **Dr. Saul Amarel**, one of the founders of the Rutgers Computer Science Department and contributor to advanced computing and artificial intelligence research and methodologies, Amarel is designed to suit many different research applications.

Through Aberdeen (late 2023):

- 560 compute nodes
 - 27,872 Intel Xeon cores
 - 224 GPUs
 - Open OnDemand servers
 - InfiniBand FDR & EDR fabric

More information:

- Community-contributed software repository
- Spans three Rutgers data centers (Piscataway, Newark, and Camden) producing a unified compute, data, and storage system
- Rolling node/phase retirement with new node replacement, beginning in spring 2021

[Click here for a short video about the Amarel cluster!](#)

Key Features of Amarel

- ① **Compute Nodes:** Amarel consists of multiple compute nodes with varying specifications, including CPUs and GPUs.
- ② **Parallel File System:** A high-speed parallel file system for storing and accessing large datasets.
- ③ **Job Scheduler:** A job scheduling system for managing computing resources efficiently.
- ④ **Software Stack:** A comprehensive collection of software packages and libraries for various scientific computing tasks.
- ⑤ **Networking:** High-speed interconnects for fast communication between compute nodes.

Getting Started with Amarel

If you are off campus, you will need access to VPN:

[Click here for Rutgers VPN instructions for Windows Users](#)

[Click here for Rutgers VPN instructions for Mac Users](#)

Getting Started with Amarel

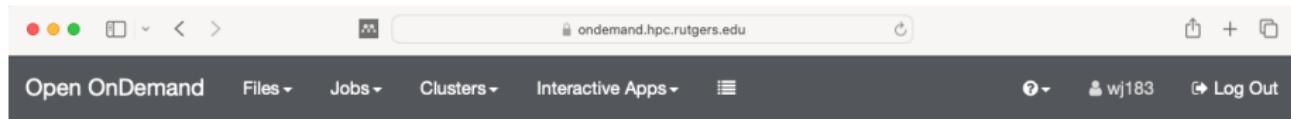
- ① **Request Access:** Contact OARC to request access to Amarel
- ② **Training Workshops:** Attend training workshops offered by OARC to learn how to use Amarel effectively.
- ③ **Documentation and Support:** Explore documentation and seek support from OARC staff and the user community.
- ④ **Start Small:** Begin with small-scale experiments and gradually scale up as needed.

Section 4

Introduction to OnDemand for HPC Clusters

What is OnDemand?

- OnDemand is a web-based platform that provides a user-friendly interface for accessing and managing (HPC) clusters.
- It simplifies the process of submitting and monitoring jobs, accessing software, and managing data on HPC systems.
- Go to: <http://ondemand.hpc.rutgers.edu> (VPN for off campus).



OPEN **OnDemand**

OnDemand provides an integrated, single access point for all of your HPC resources.

powered by

OnDemand

Key Features of OnDemand

- ① **Web Interface:** Access HPC resources through a web browser from anywhere with an internet connection.
- ② **Job Submission:** Submit and manage computational jobs without needing to use command-line interfaces.
- ③ **File Management:** Upload, download, and manage files and data on the HPC cluster directly from the browser.
- ④ **Interactive Sessions:** Launch interactive computing sessions for data analysis and exploration.
- ⑤ **Software Environment:** Access a variety of software packages and development tools installed on the HPC cluster.

Benefits of OnDemand

- **User-Friendly:** OnDemand provides a simplified interface, making HPC resources more accessible to a wider range of users.
- **Remote Access:** Users can access HPC resources remotely without needing to install any special software.
- **Increased Productivity:** Streamlined workflows and intuitive interfaces help users focus on their research instead of dealing with technical complexities.

Accessing Files

The screenshot shows the File Explorer v1.4.1 interface. At the top, there are buttons for Dashboard, Go To..., Open in Terminal, New File, New Dir, Upload, Show Dotfiles, Show Owner/Mode, and a search bar for File Explorer - /home/wj183/. Below the toolbar is a sidebar titled "Home Directory" containing links to various directories: 2023_03_ugandan_nasal_blood, Desktop, Documents, Downloads, Music, Pictures, Public, R, Templates, Videos, bin, for_howard, intel, my.R.libs, ondemand, rna_seq, and wejlab. The main area displays the contents of the current directory, /home/wj183/, in a table format. The table has columns for name, size, and modified date. The table includes entries for .., 2023_03_ugandan_nasal_blood, Desktop, Documents, Downloads, Music, Pictures, Public, R, Templates, Videos, bin, for_howard, intel, my.R.libs, ondemand, rna_seq, wejlab, basespace_example.sh, and for_howard.zip. The file for_howard.zip is highlighted with a red border.

name	size	modified date
..	<dir>	03/31/2023
2023_03_ugandan_nasal_blood	<dir>	03/27/2023
Desktop	<dir>	03/21/2023
Documents	<dir>	03/21/2023
Downloads	<dir>	03/21/2023
Music	<dir>	03/21/2023
Pictures	<dir>	03/21/2023
Public	<dir>	03/21/2023
R	<dir>	03/31/2023
Templates	<dir>	03/21/2023
Videos	<dir>	03/21/2023
bin	<dir>	03/21/2023
for_howard	<dir>	07/26/2023
intel	<dir>	03/31/2023
my.R.libs	<dir>	03/31/2023
ondemand	<dir>	11/14/2022
rna_seq	<dir>	03/31/2023
wejlab	<dir>	03/07/2024
basespace_example.sh	87b	03/27/2023
for_howard.zip	4.87gb	07/26/2023

Accessing the Terminal

The screenshot shows the OnDemand web interface with a terminal session open. The top navigation bar includes links for Open OnDemand, Files, Jobs, Clusters, Interactive Apps, and Log Out. A dropdown menu under Clusters is open, showing options like Amarel Cluster Shell Access and Amarell Amarel Cluster Shell Access | Access. The main content area features the OnDemand logo and a message stating "OnDemand provides an integrated, single access point for all of your HPC resources." Below this is a terminal window with the following content:

```
wj183@amarell.hpc.rutgers.edu's password:  
#  
AMAREL AT RUTGERS  
Welcome to the AMAREL research computing cluster managed by  
the Office of Advanced Research Computing (OARC) at Rutgers University  
http://oarc.rutgers.edu  
Need help? Send an e-mail to help@oarc.rutgers.edu  
User documentation: https://sites.google.com/view/cluster-user-guide  
Do NOT run programs, tests, analyses, or pre/postprocessing on the shared  
login nodes (amarell1, amarell2, etc.). That's what compute nodes are for.  
#[wj183@amarell1 ~]$ #
```

Accessing the Amarel Desktop through OnDemand

The screenshot shows the OnDemand web interface. At the top, there is a navigation bar with links for "Open OnDemand", "Files", "Jobs", "Clusters", "Interactive Apps", and "Log Out". Below the navigation bar, the main content area features the "OnDemand" logo with a "OPEN" button. A sub-section titled "OnDemand provides an integrated,..." is visible. To the right of the logo, a sidebar lists various desktop and server options. The "Amarel Desktop" option is highlighted with a blue border, indicating it is selected. Other listed options include "OARC Advanced Desktop" and "Sirius3 Desktop" under Desktops; and "Comp. Gen. Jupyter", "Gen303 - RStudio", "Jupyter Notebook 2", "Jupyter Notebook 3", "Jupyter for GEN203 class", "MATLAB", "Personal Jupyter", "RStudio Server", and "Test for GEN203 class" under Servers.

OPEN

OnDemand

OnDemand provides an integrated, ...

Interactive Apps

RNA Seq Batch Job

cellranger

cellranger-aggr

cellranger-fastq2count

cellranger-mkfastq

Desktops

Amarel Desktop

OARC Advanced Desktop

Sirius3 Desktop

Servers

Comp. Gen. Jupyter

Gen303 - RStudio

Jupyter Notebook 2

Jupyter Notebook 3

Jupyter for GEN203 class

MATLAB

Personal Jupyter

RStudio Server

Test for GEN203 class

Accessing the Amarel Desktop through OnDemand

Open OnDemand Files ▾ Jobs ▾ Clusters ▾ Interactive Apps ▾ ☰ ? ▾ wj183 Log Out

Home / My Interactive Sessions / Amarel Desktop

Interactive Apps

Desktops

Amarel Desktop

OARC Advanced Desktop

Sirius3 Desktop

Servers

Comp. Gen. Jupyter

Gen303 - RStudio

Jupyter Notebook 2

Jupyter Notebook 3

Jupyter for GEN203 class

MATLAB

Personal Jupyter

RStudio Server

Test for GEN203 class

Amarel Desktop

This app will launch an interactive desktop on one or more compute nodes. You will have full access to the resources these nodes provide. This is analogous to an interactive batch job.

Number of hours

12

Num Cores

Gigabytes of memory

4

Number of gigabytes of memory (larger values may mean longer wait)

Partition

Reservation

Launch

Accessing the Amarel Desktop through OnDemand

[Open OnDemand](#)[Files](#) ▾[Jobs](#) ▾[Clusters](#) ▾[Interactive Apps](#) ▾[?](#) ▾[wj183](#)[Log Out](#)

Session was successfully created.

[Home](#) / My Interactive Sessions

Interactive Apps
Desktops
Amarel Desktop
OARC Advanced Desktop
Sirius3 Desktop
Servers
Comp. Gen. Jupyter
Gen303 - RStudio
Jupyter Notebook 2
Jupyter Notebook 3
Jupyter for GEN203 class
MATLAB
Personal Jupyter
RStudio Server
Test for GEN203 class

Amarel Desktop (36349078)

Queued

Created at: 2024-04-29 10:51:36 EDT

 [Delete](#)

Time Requested: 12 hours

Session ID: d6886f60-dd03-4dad-b856-8f02e081f209

Please be patient as your job currently sits in queue. The wait time depends on the number of cores as well as time requested.

Accessing the Amarel Desktop through OnDemand

Open OnDemand Files ▾ Jobs ▾ Clusters ▾ Interactive Apps ▾ ? ▾ wj183 Log Out

Session was successfully created.

Home / My Interactive Sessions

Interactive Apps

- Desktops
 - Amarel Desktop
 - OARC Advanced Desktop
 - Sirius3 Desktop
- Servers
 - Comp. Gen. Jupyter
 - Gen303 - RStudio
 - Jupyter Notebook 2
 - Jupyter Notebook 3
 - Jupyter for GEN203 class
 - MATLAB
 - Personal Jupyter
 - RStudio Server
 - Test for GEN203 class

Amarel Desktop (36349078) 1 node | 1 core | Running

Host: hal0005.amarel.rutgers.edu Delete

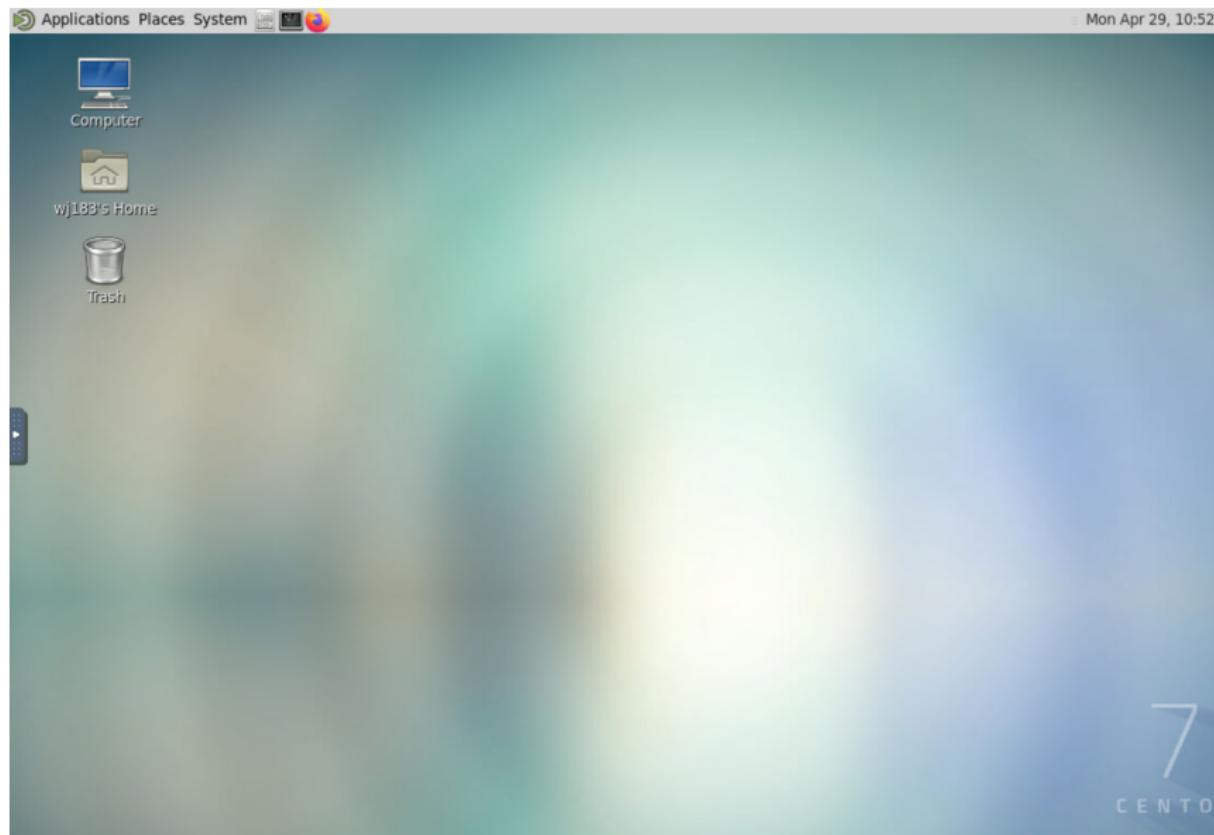
Created at: 2024-04-29 10:51:36 EDT

Time Remaining: about 12 hours

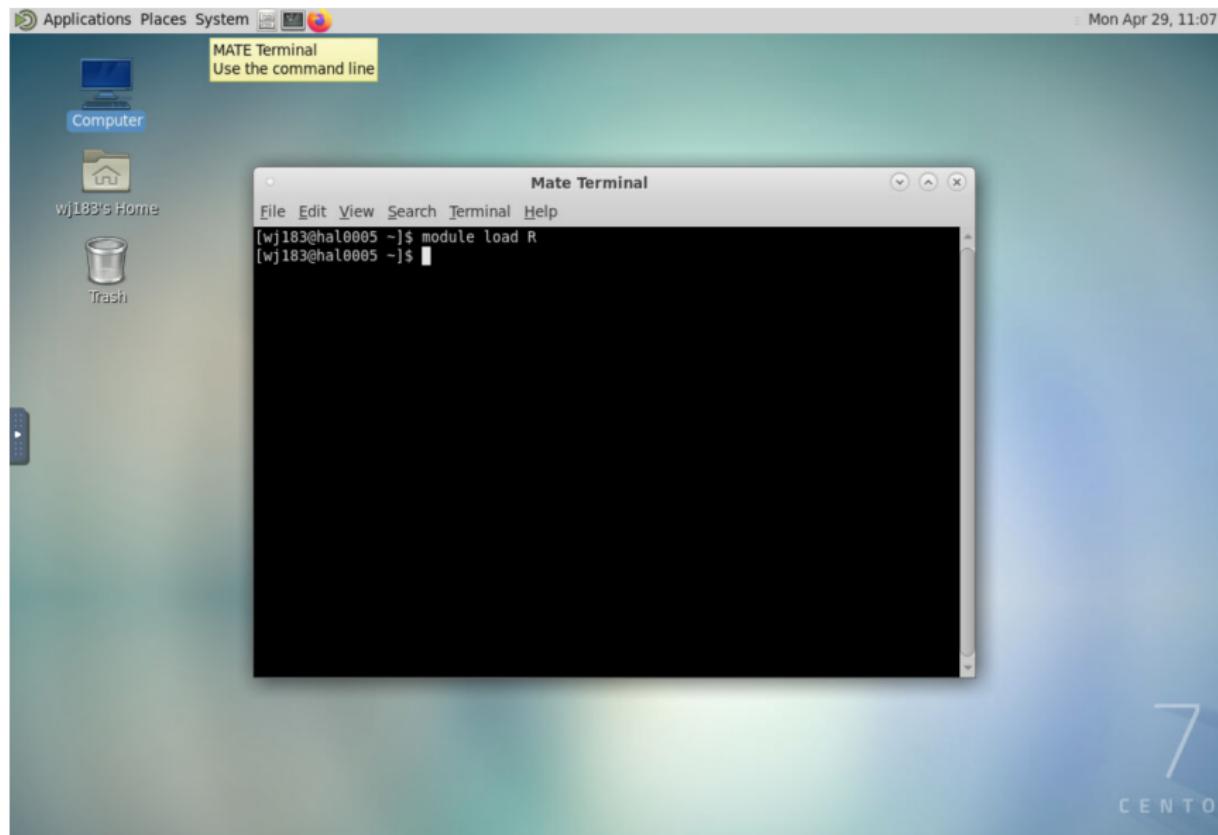
Session ID: d6886f60-dd03-4dad-b856-8f02e081f209

Launch noVNC in New Tab View Only (Share-able Link)

Accessing the Amarel Desktop through OnDemand



Accessing the Amarel Desktop through OnDemand



Accessing R through the terminal

You first need to attach R to your session (using Amarel Desktop):

```
[wj183@hal0005 ~]$ module load R  
[wj183@amarel1 ~]$ R
```

Accessing the RStudio through OnDemand

The screenshot shows the OnDemand web interface. At the top, there's a navigation bar with links for "Open OnDemand", "Files", "Jobs", "Clusters", "Interactive Apps", "Log Out", and a user profile for "wj183". The main content area has a large "OPEN OnDemand" logo. Below it, a text block says "OnDemand provides an integrated, unified interface to all of your HPC resources." To the right, a sidebar lists various interactive applications under categories like Desktops and Servers. The "Interactive Apps" menu is open, showing options such as "RNA Seq Batch Job", "cellranger", "cellranger-aggr", "cellranger-fastq2count", "cellranger-mkfastq", "Desktops" (listing Amarel Desktop, OARC Advanced Desktop, Sirius3 Desktop), "Servers" (listing Comp. Gen. Jupyter, Gen303 - RStudio, Jupyter Notebook 2, Jupyter Notebook 3, Jupyter for GEN203 class, MATLAB, Personal Jupyter, RStudio Server, and Test for GEN203 class). The "RStudio Server" option is highlighted with a gray background.

OnDemand provides an integrated, unified interface to all of your HPC resources.

Interactive Apps

- RNA Seq Batch Job
- cellranger
- cellranger-aggr
- cellranger-fastq2count
- cellranger-mkfastq

Desktops

- Amarel Desktop
- OARC Advanced Desktop
- Sirius3 Desktop

Servers

- Comp. Gen. Jupyter
- Gen303 - RStudio
- Jupyter Notebook 2
- Jupyter Notebook 3
- Jupyter for GEN203 class
- MATLAB
- Personal Jupyter
- RStudio Server
- Test for GEN203 class

powered by

OPEN **OnDemand**

Accessing the RStudio through OnDemand

Open OnDemand Files ▾ Jobs ▾ Clusters ▾ Interactive Apps ▾ wj183 Log Out

Home / My Interactive Sessions / RStudio Server

Interactive Apps

- Desktops
- Amarel Desktop
- OARC Advanced Desktop
- Sirius3 Desktop
- Servers
- Comp. Gen. Jupyter
- Gen303 - RStudio
- Jupyter Notebook 2
- Jupyter Notebook 3
- Jupyter for GEN203 class
- MATLAB
- Personal Jupyter
- RStudio Server
- Test for GEN203 class

RStudio Server

This app will launch [RStudio Server](#) an IDE for R on the [Amarel](#) cluster.

Partition

nonpre

- nonpre - nonpreemptible partition (a subset of nodes that are community owned)
- main - all nodes, including owners
- graphical - single node dedicated to small interactive jobs (2 cores, 4G RAM maximum)

R version

RStudio with R version 3.5.2

This defines the version of R you want to load.

Number of hours

12

Number of cores

1

Number of cores on node type (4 GB per core)

Launch

* All RStudio Server session data is generated and stored under the user's home directory in the corresponding data root directory.

Accessing the RStudio through OnDemand

[Open OnDemand](#)[Files](#) ▾[Jobs](#) ▾[Clusters](#) ▾[Interactive Apps](#) ▾[?](#) ▾[wj183](#)[Log Out](#)

Session was successfully created.

[Home](#) / [My Interactive Sessions](#)

Interactive Apps
Desktops
Amarel Desktop
OARC Advanced Desktop
Sirius3 Desktop
Servers
Comp. Gen. Jupyter
Gen303 - RStudio
Jupyter Notebook 2
Jupyter Notebook 3
Jupyter for GEN203 class
MATLAB
Personal Jupyter
RStudio Server
Test for GEN203 class

RStudio Server (36349030)

Queued

Created at: 2024-04-29 10:29:19 EDT [Delete](#)**Time Requested:** 12 hours**Session ID:** [a26538a5-1a7d-41d8-b74c-093795747c2a](#)

Please be patient as your job currently sits in queue. The wait time depends on the number of cores as well as time requested.

Accessing the RStudio through OnDemand

[Open OnDemand](#)[Files](#) ▾[Jobs](#) ▾[Clusters](#) ▾[Interactive Apps](#) ▾

wj183

[Log Out](#)

Session was successfully created.

[Home](#) / [My Interactive Sessions](#)**Interactive Apps**

Desktops

Amarel Desktop

OARC Advanced Desktop

Sirius3 Desktop

Servers

Comp. Gen. Jupyter

Gen303 - RStudio

Jupyter Notebook 2

Jupyter Notebook 3

Jupyter for GEN203 class

MATLAB

Personal Jupyter

RStudio Server

Test for GEN203 class

RStudio Server (36349030)

1 node | 1 core | Running

Host: hal0100.amarel.rutgers.edu

Delete

Created at: 2024-04-29 10:29:19 EDT**Time Remaining:** about 12 hours**Session ID:** a26538a5-1a7d-41d8-b74c-093795747c2a

Connect to RStudio Server

Accessing the RStudio through OnDemand

The screenshot shows the RStudio interface running on an OnDemand session. The top bar indicates the session is connected to `wj183@amarefti:`. The left sidebar shows several open files: `takeHome.Rmd`, `unix.Rmd`, `Untitled1`, and `indices.R`. The main workspace shows an empty Environment pane with the message "Environment is empty". The right sidebar displays a file tree under the "Home" directory, showing files like `2023_03_ugandan_nasal_blood`, `basespace_example.sh`, `bin`, `Desktop`, `Documents`, `Downloads`, `for_howard`, `for_howard.zip` (4.9 GB, modified Jul 26, 2023, 7:12 PM), `intel`, `Music`, `my.R.libs`, `ondemand`, `Pictures`, `Public`, and `R`. The bottom left shows the console output:

```
1:1 (Top Level) R Script
Console Terminal
~/
*** installing help indices
** building package indices
** installing vignettes
** testing if installed package can be loaded
* DONE (Rsubread)

The downloaded source packages are in
'/tmp/Rtmp5arkZ9/downloaded_packages'
Installation paths not writeable, unable to update packages
  path: /usr/lib/R/library
  packages:
```

Section 5

Introduction to Cluster Batch Job Scheduling with SLURM

What is SLURM?

- SLURM (Simple Linux Utility for Resource Management) is an open-source job scheduler and resource manager used on many high-performance computing (HPC) clusters.
- It allows users to submit, manage, and monitor batch jobs on computing clusters efficiently.

Key Concepts

- ① **Partition:** A partition is a logical grouping of compute nodes with similar hardware characteristics or usage policies.
- ② **Job Script:** A job script is a text file containing instructions for the scheduler, including job parameters, resource requests, and executable commands.
- ③ **Resource Allocation:** Users specify the required resources for their jobs, such as CPUs, memory, and runtime, in the job script.
- ④ **Job Status:** Users can monitor the status of their submitted jobs, including waiting, running, completed, or failed, using SLURM commands or monitoring tools.

Submitting a Job with SLURM

- ① **Create a Job Script:** Write a job script using a text editor, specifying job parameters and commands.
- ② **Submit the Job:** Use the `sbatch` command to submit the job script to SLURM.
- ③ **Monitor Job Status:** Check the status of the submitted job using commands like `squeue` or monitoring tools provided by SLURM.
- ④ **Retrieve Results:** Once the job completes, retrieve the results and data generated by the job from the designated output directory.

Example Job Script

```
#!/bin/bash
#SBATCH --job-name=my_job
#SBATCH --nodes=1
#SBATCH --ntasks-per-node=4
#SBATCH --mem=8G
#SBATCH --time=1:00:00

# Execute your command here
./my_executable input_file.txt > output_file.txt
```

Best Practices

- Resource Requests: Specify accurate resource requirements to ensure optimal resource allocation and job performance.
- Job Prioritization: Understand the partition structure and prioritize jobs accordingly to optimize resource utilization.
- Job Dependencies: Use job dependencies to sequence jobs and ensure proper execution order when necessary.
- Error Handling: Include error handling and logging mechanisms in job scripts to facilitate troubleshooting and debugging.

Conclusion

SLURM is a powerful tool for managing batch job scheduling and resource allocation on cluster computing systems. By understanding key concepts and following best practices, users can effectively utilize SLURM to submit, manage, and monitor computational tasks on HPC clusters. Explore documentation and seek support from the cluster administrators or user community to learn more about SLURM and optimize your workflow.

Next Lecture: Git and GitHub

For the next lecture you will need to install git and get a GitHub account.

To install git on Windows, install GitBash. Visit the official Git website: <https://git-scm.com/>, and then click on the “Download for Windows” button.

To install git on Mac, follow these instructions:
<https://git-scm.com/downloads/mac>

Next Lecture: Git and GitHub

After installing git, go get a GitHub account. Go to <https://github.com/>. You will see a link to sign up in the top right corner.

Pick a name carefully! Something short, related to your name, and professional. Remember that you will use this to share code with others. You might be sharing this with potential collaborators or future employers!

Session info

```
sessionInfo()
```

```
## R version 4.5.1 (2025-06-13)
## Platform: aarch64-apple-darwin20
## Running under: macOS Tahoe 26.2
##
## Matrix products: default
## BLAS:    /Library/Frameworks/R.framework/Versions/4.5-arm64/Resources/lib/libRblas.0.dylib
## LAPACK:  /Library/Frameworks/R.framework/Versions/4.5-arm64/Resources/lib/libRlapack.dylib;  LAPACK version 3
##
## locale:
## [1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8
##
## time zone: America/Denver
## tzcode source: internal
##
## attached base packages:
## [1] stats      graphics   grDevices utils      datasets   methods    base
##
## loaded via a namespace (and not attached):
## [1] compiler_4.5.1    fastmap_1.2.0    cli_3.6.5       tools_4.5.1
## [5] htmltools_0.5.9   otel_0.2.0     rstudioapi_0.17.1 yaml_2.3.12
## [9] rmarkdown_2.30    knitr_1.51     xfun_0.55      digest_0.6.39
## [13] rlang_1.1.6      evaluate_1.0.5
```